

1   tgagggcgcc atgaggagcc tgtgtgcgcc ccactcctg ctctcttgc tgctgccgcc  
61   gctgtgctc acgccccgcg ctggggacgc cgccgtgac accggggcct gtgacaagga  
121   ctcccaatgt ggtggaggca tgtgtgtgc tgtcagtatc tgggtcaaga gcataaggat  
181   ttgcacacct atgggcaaac tgggagacag ctgccatcca ctgactcgta aaaacaattt  
241   tggaaatgga aggcaggaaa gaagaaagag gaagagaagc aaaaggaaaa aggaggttcc  
301   atTTTTTggg cggaggatgc atcacacttg ccattgtctg ccaggcttgg cctgtttacg  
361   gacttcattt aaccgattta ttgttttagc ccaaaagtaa tcgctctgga gtagaaacca  
421   aatgtga

## FIGURE 1

MRSI CCAP L L L L L P P L L L T P R A G D A A V I T G A C D K D S Q C G G G M C C A V S I W V K S I R I C T  
P M G K L G D S C H P L T R K N N F G N G R Q E R R K R K R K K E V P F F G R R M H H T C P C L P G L A C L R T  
S F N R F I C L A Q K

## FIGURE 2

1   tgagggcgcc atgaggagcc tgtgctgcg ccactcctg ctctcttgc tgctgccgcc  
61   gagggcgcca tgaggagcct gtgctgcgcc ccactcctgc tcctcttgc tctgccgccg  
121   ctgctgctca cgccccgcgc tggggacgcc gccgtgatca ccggggcttg tgacaaggac  
181   tcccaatgtg gtggaggcat gtgctgtgct gtcagtatct gggtaagag cataaggatt  
241   tgcacaccta tgggcaact gggagacagc tgccatccac tgactcgtaa agttccattt  
301   tttgggcgga ggatgcatca cacttgcca tgtctgccag gcttggcctg ttacgggact  
361   tcatttaacc gatttatttg tttagcccaa aagtaatcgc tctggagtag aaaccaaagt  
421   tga

**FIGURE 3**

MRSLCCAPLLLLLLLLPPLLLTPRAGDAAVITGACDKDSQCGGGMCCAVSIWVKSIRICT  
PMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLACLRTSFNRFCILAQK

**FIGURE 4**

1 cggacgcgtg ggcgtccctt aaccgccacc gcgtccccgg gacgcatgg gggacccgcg  
 61 ctgtgccccg ctactgctac ttctgtgctt accgtgctg ttacacccgc ccgcccgggga  
 121 tgccgcggtc atcacccggg cttgcgacaa ggactctcag tgcggaggag gcatgtgctg  
 181 tgctgtcagt atctggggtta agagcataag gatctgcaca cctatgggcc aagtgggcga  
 241 cagctgccac cccctgactc ggaagttcc atttggggg cggaggatgc accacacctg  
 301 cccctgcctg ccaggccttg cgtgtttaag gacttcttc aaccggttta ttgcttgcc  
 361 ccggaatga tcaactctgaa gtaggaactt gaaatgcgac cctccgctgc acaatgtccg  
 421 tcgagtctca cttgtaattg tggcaaacaa agaatactcc agaaagaaat gtctcccccc  
 481 ttccctgact ttccaagtaa cgtttctatc tttgattttt gaagtggctt tttttttttt  
 541 ttttttttcc ttcccttgaa ggaagtttt gatttttgga gagattata gaggactttc  
 601 tgacatggct tctcatttcc ctgtttatgt ttgacctga catttttgaa tgccaataac  
 661 aactgttttc acaaatagga gaataagagg gaacaatctg ttgcagaaac ttcccttttg  
 721 cctttgcccc actcgccccg cccgccccg ccccgccctg cccatgcgca gacagacaca  
 781 cccttactct tcaagactc tgatgatcct caccttactg tagcattgtg ggtttctaca  
 841 ctccccccg ccctggttg accactgag gaggctcaga gagctagcac tgtacagggt  
 901 tgaaccagat cccccaagca gctcatttg ggcagacgtt gggagcgctc caggaaacttt  
 961 cctgcaccca tctggccac tggctttcag ttctgctgtt taactgggtg gaggacaaaa  
 1021 ttaacgggac cctgaaggaa cctggcccg ttatctagat ttgtttaagt aaaagacatt  
 1081 ttctccttgt tgtggaatat tacatgtctt tttctttttt atctgaagct tttttttttt  
 1141 ttctttaagt cttcttgttg gagacatttt aaagaacgcc actcgaggaa gcattgattt  
 1201 tcatytgga tgacaggagt catcatttta aaaaatcgggt gttaagttat aatttaaaact  
 1261 ttatttgtta cccaaaggtg taatgtaaat ggatttcctg atatcctgcc atttgtactg  
 1321 gatatcaatat ttttatgt

FIGURE 5

MGDPRCAPLLLLLLPPLFFTPAGDAAVITGACDKDSQCGGMCCAVSIWKSIRICTP  
MGQVGDSCHPLTRKVPFWGRRMHHTCPCLPGLACLRTSFNRFICLARK

**FIGURE 6**

Human BV8	10	20	30	40	50
Mouse BV8	<u>MRSLCCAPLLLLLLLLLPPLLLTPPRAGDAAVITGACDKDSQCGGMCCAVSI</u> <u>MGDPRCAPLLLLLLLLLPPLLLFTTPRAGDAAVITGACDKDSQCGGMCCAVSI</u>				
Human BV8	60	70	80	90	100
Mouse BV8	WVKSIRICTPMGKLGDSCHPLTRKNNFGNGRQERRRKRKRKRKEVPFF-G WVKSIRICTPMGVGDSCHPLTRKSHVANGROERRRAKRRKRKEVVPFWG				
Human BV8	110	120	129		
Mouse BV8	RRMHHTCPCLPGLACLRTSFNRFICLAQK RRMHHTCPCLPGLACLRTSFNRFICLARK				

FIGURE 7

```

1  tggcctcccc agcttgccag gcacaaggct gagcgggagg aagcgagagg catctaagca ggcagtgttt
71  tgccttcacc ccaagtgacc atgagagggtg ccacgcgagt ctcaatcatg ctctctctag taactgtgtc
141  tgactgtgct gtgatcacag gggcctgtga ggggatgtc cagtgtggg caggcacctg ctgtgccatc
211  agcctgtggc ttcgaggggt gcggatgtgc accccgctgg ggcgggaagg cgaggagtgc caccocggca
281  gccacaaggt ccccttcttc aggaacgca agcaccacac ctgtccttgc ttgcccacac tgctgtgtc
351  caggttcccg gacggcaggt accgtgtgc catggacttg aagaacatca attttaggc gcttgccctgg
421  tctcaggata ccaccatcc ttttcctgag cacagcctgg atttttattt ctgccatgaa acccagctcc
491  catgactctc ccagtcccta cactgactac cctgactctc cttgtctagt acgcacatat gcacacaggc
561  agacatacct cccatcatga catggtcccc aggcctggcct gaggatgtca cagcttgagg ctgtggtgtg
631  aaagggtggc agcctgttct tcttcctgc tcaggctgcc agagaggtgg taaatggcag aaaggacatt
701  cccctcccc tccccaggtg acctgtctct tttcctgggc cctgccccct tccccacatg tatccctcgg
771  tctgaattag acattcctgg gcacaggctc ttgggtgcat tgctcagagt ccaggtcctt ggcctgaccc
841  tcaggccctt cacgtgaggt ctgtgaggac caatttgttg gtagttcatc ttccctcgat tggttaactc
911  cttagtttca gaccacagac tcaagattgg ctcttcccag agggcaggag acagtcaccc caaggcaggt
981  gtagggagcc cagggaggcc aatcagcccc ctgaagactc tggctccagt cagcctgttg ctgttgccct
1051  gtgacctgtg accttctgcc agaattgtca tgcctctgag gccccctctt accacacttt accagttaac
1121  cactgaagcc cccaattccc acagcttttc cattaaaaatg caaatggtgg tggttcaatc taatctgata
1191  ttgacatatatt agaaggcaat taggggtgtt ccttaaaaaa ctcttttcca aggatcagcc ctgagagcag
1261  gttggtgact ttgaggaggg cagtcctctg tccagattgg ggtgggagca agggacagg agcagggcag
1331  gggctgaaag gggcactgat tcagaccagg gaggcaacta cacaccaaca tgctggcttt agaataaaa
1401  caccaactga aaaa.

```

FIGURE 8



Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Val Thr Val Ser  
 10  
 20  
 Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala  
 30  
 Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr  
 40  
 50  
 Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val Pro  
 60  
 70  
 Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu Leu  
 80  
 90  
 Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn  
 100  
 105  
 Ile Asn Phe

Figure 9

```

1   GAA GTG AGG GGT ACC AAA GTA GAC TGT GTT TGT CGT CAC CTC AAG TGA TC

51  ATG AGA GGC GCT GTG CAT ATC TTC ATC ATG CTC CTT CTA GCA ACG GCG TCC
    M R G A V H I F I M L L L A T A S

102 GAC TGT GCG GTC ATC ACA GGG GCC TGT GAA CGA GAT ATC CAG TGT GGG GCC
    D C A V I T G A C E R D I Q C G A

153 GGC ACC TGC TGC GCT ATC AGT CTG TGG CTG CGG GGC CTG CGG TTG TGT ACC
    G T C C A I S L W L R G L R L C T

204 CCA CTG GGG CGT GAA GGA GAG TGC CAC CCA GGA AGC CAC AAG ATC CCC
    P L G R E G E C H P G S H K I P

255 TTC TTG AGG AAA CGC CAA CAC CAT ACC TGT CCC TGC TCA CCC AGC CTG CTG
    F L R K R Q H H T C P C S P S L L

306 TGC TCC AGG TTC CCG GAC GGC AGG TAC CGC TGC TTC CGG GAC TTG AAG AAT
    C S R F P D G R Y R C F R D L K N

357 GCC AAC TTT TAGTTTGTCTGGACTCTGTCTGGAGCCTGACTGGGTGACCTCTTGCTTTACACCT
    A N F *

GTGTGATTTAGCTCCCTGCAACTTCGCCATTCCCATCTTGTCCGTGTATGTGCAGACAGGCAGACC
TTCCGCTATGGAATAGTTTCAACAGGGTGACAGAGAGTTCGTGGCCTTGAGAAAGTTGGCCAGCCCG
ACCTTCCTGGCTCAGACTGCCCTGAAGTTGTGACAGTGTGGCCCTTCTCAGTTGCCCTGCCCTTCCTG
CATGTGGCCTTCTTCCCTAAACACACACCTTTCTGGGCACTGGCCCATGGATGCACCACTAAATCAACA
GGTCTGTGGGTGGATGATCAACTTCTCTCCATTTTCTTTTATTGACTGGCTTCCTAATTTAAGG
ACTGT

```

Figure 10

human	EG-VEGF	MRGATRVSIM	LLLVTVSDCA	VITGACERDV	QCGAGTCCAI	SLWLRGLRMC	50
murine	EG-VEGF	MKGAVHIFIM	LLLATASDCA	VITGACERDI	QCGAGTCCAI	SLWLRGLRLC	
human	EG-VEGF	TPLGREGEEC	HPGSHKVPFF	RKRKHHTCPC	LPNLLCSRFP	DGRYRCSMDL	100
murine	EG-VEGF	TPLGREGEEC	HPGSHKIPFL	RKRQHHTCPC	SPSLLCSRFP	DGRYRCFRDL	105

Figure 11

Human BV8	28	AVITGACDKDSQCGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPF
	20	
Human EG-VEGF		AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHPGSHKVPF
	78	
Human Bv8	108	FGRRMHTCPCLPGLACLRTSFNRFICLAQK
	70	
Human EG-VEGF	105	FRKRKHTCPCLPNLLCSRFDPGRYRCSMDLKNINF

## FIGURE 12

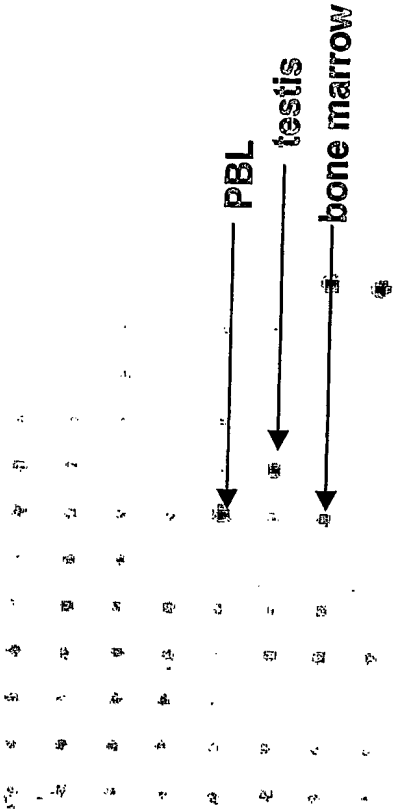


FIGURE 13

tonsillitis

appendicitis

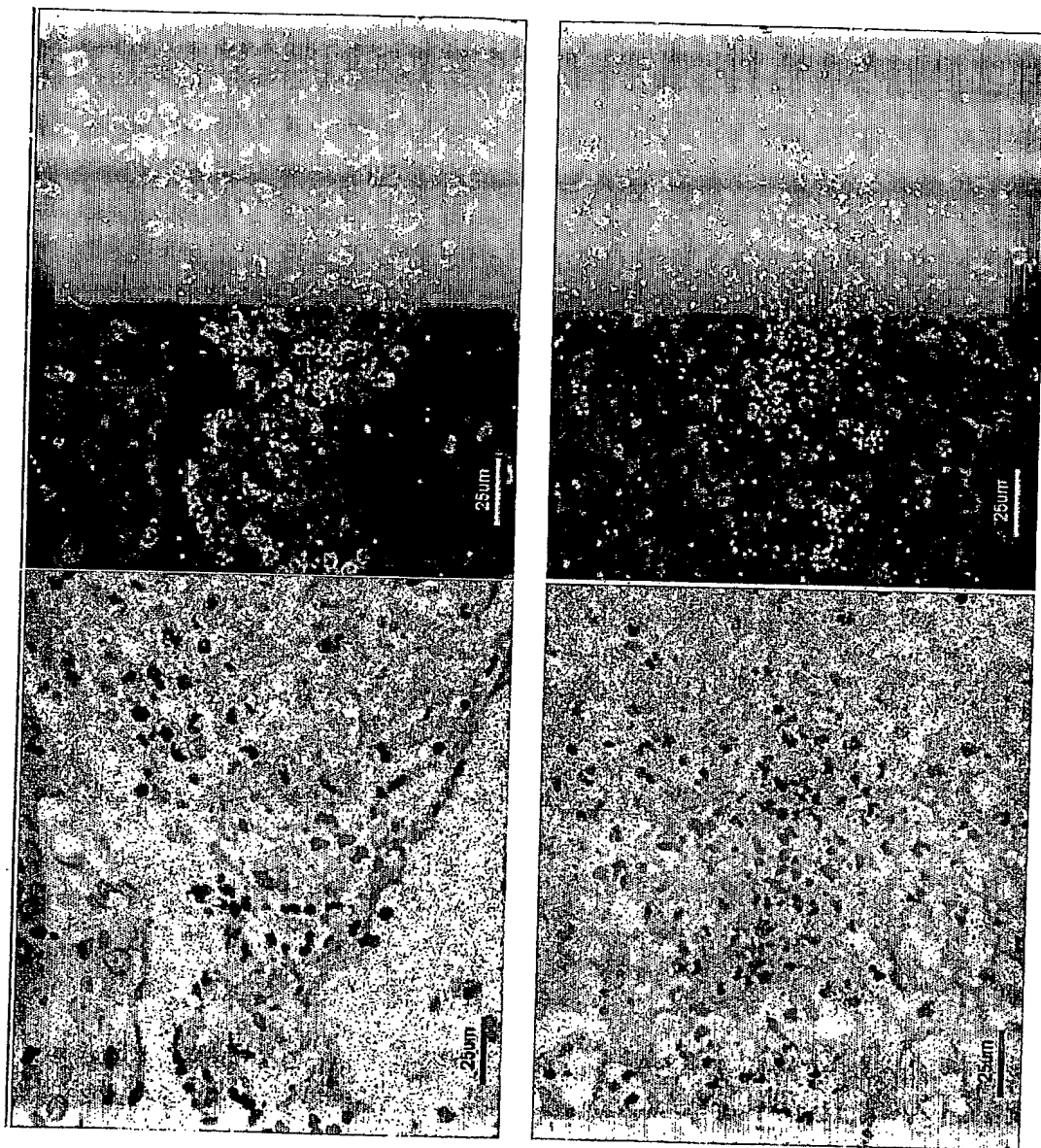
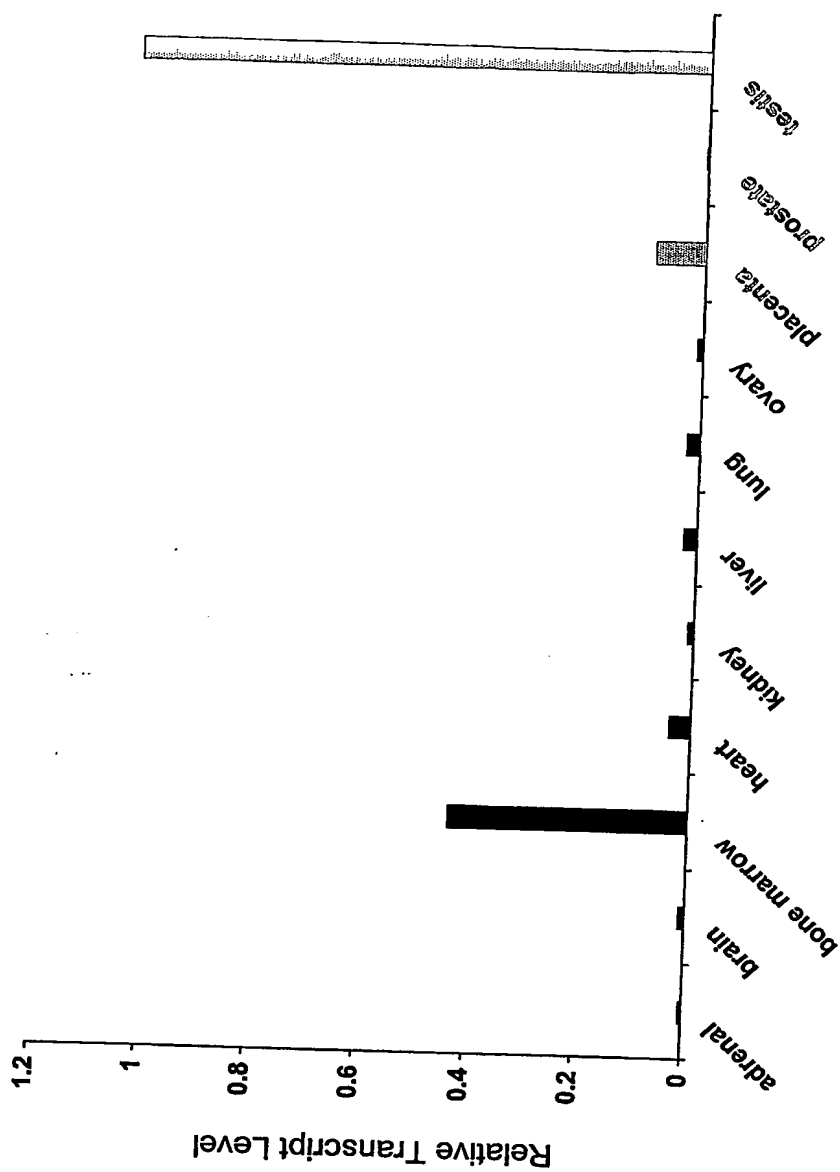


FIGURE 14

**FIGURE 15A**

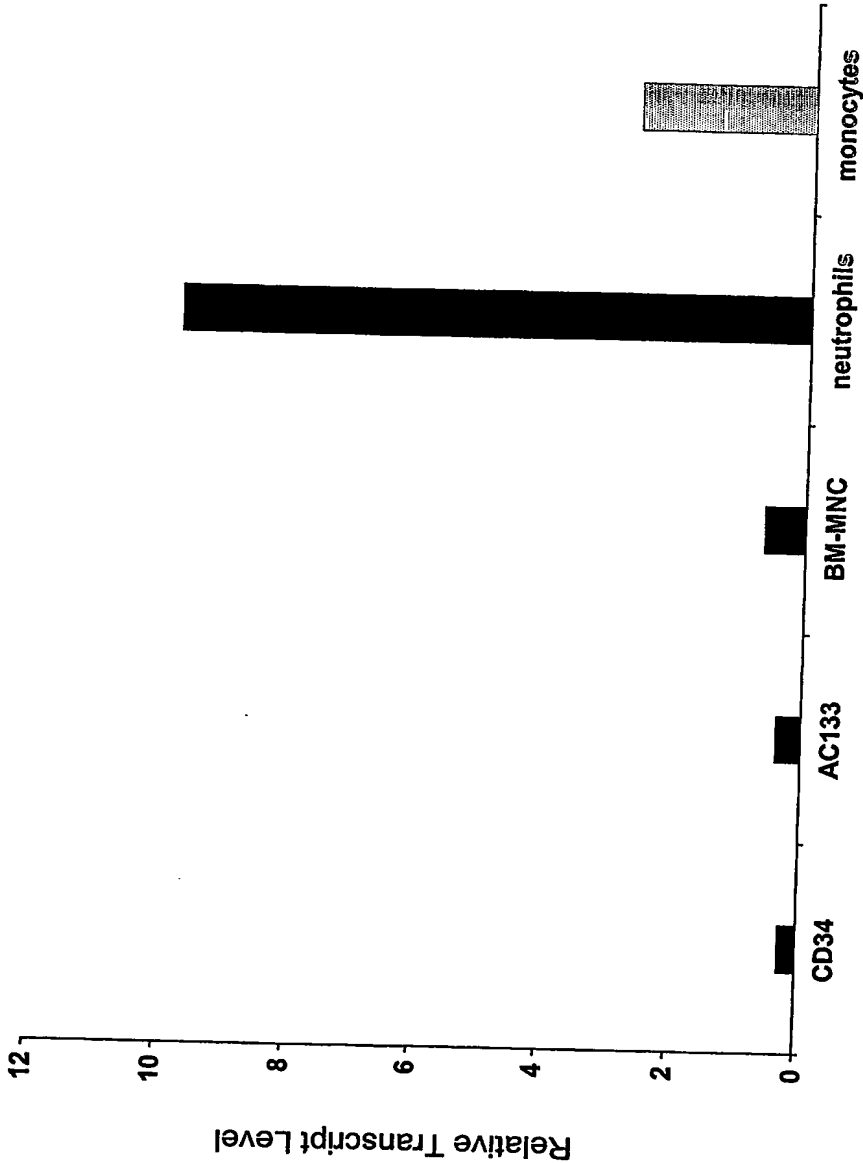
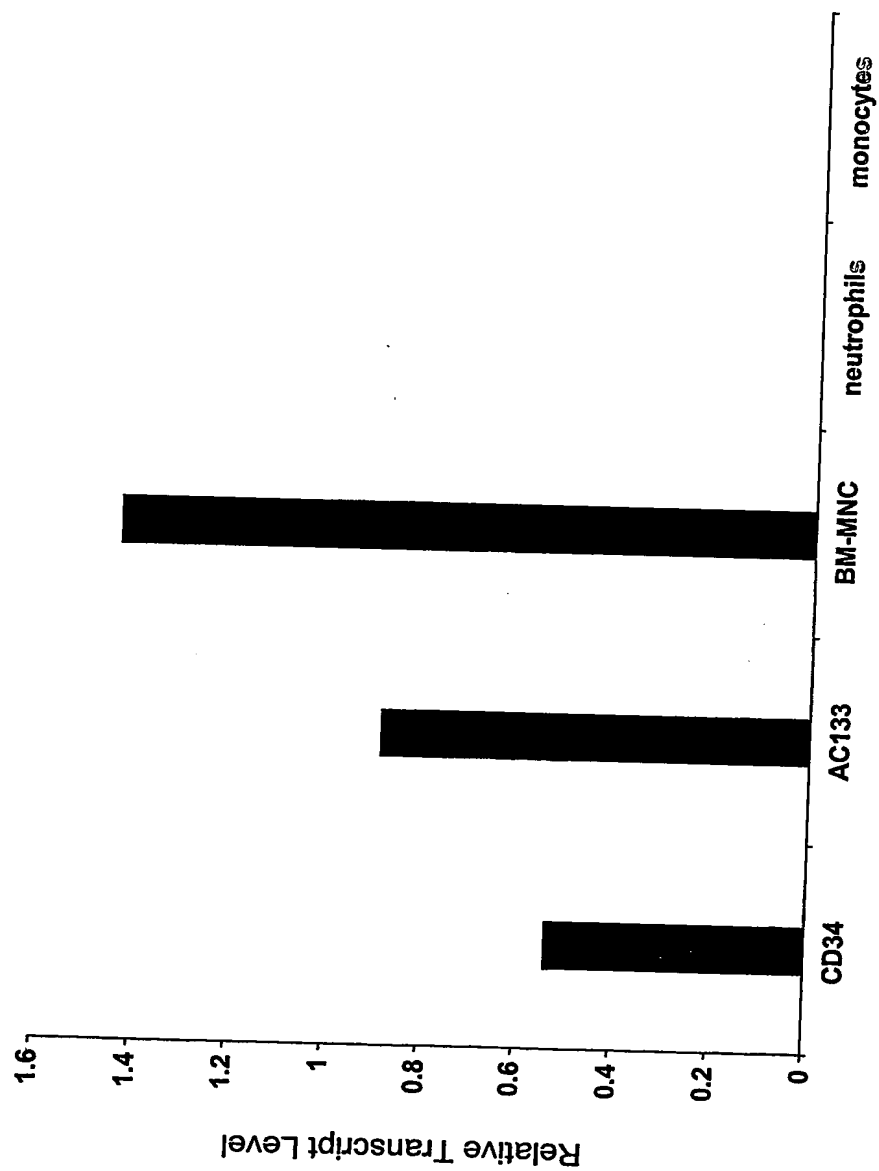


FIGURE 15B



**FIGURE 15C**

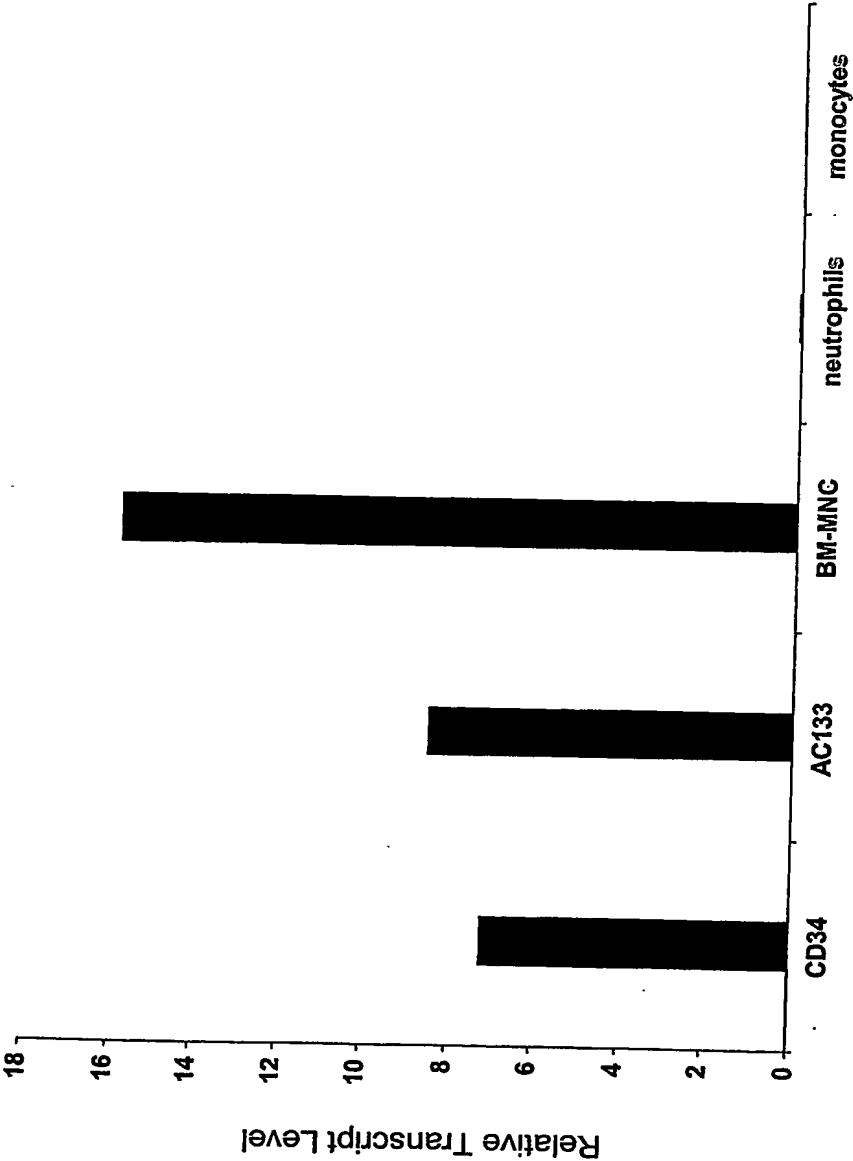
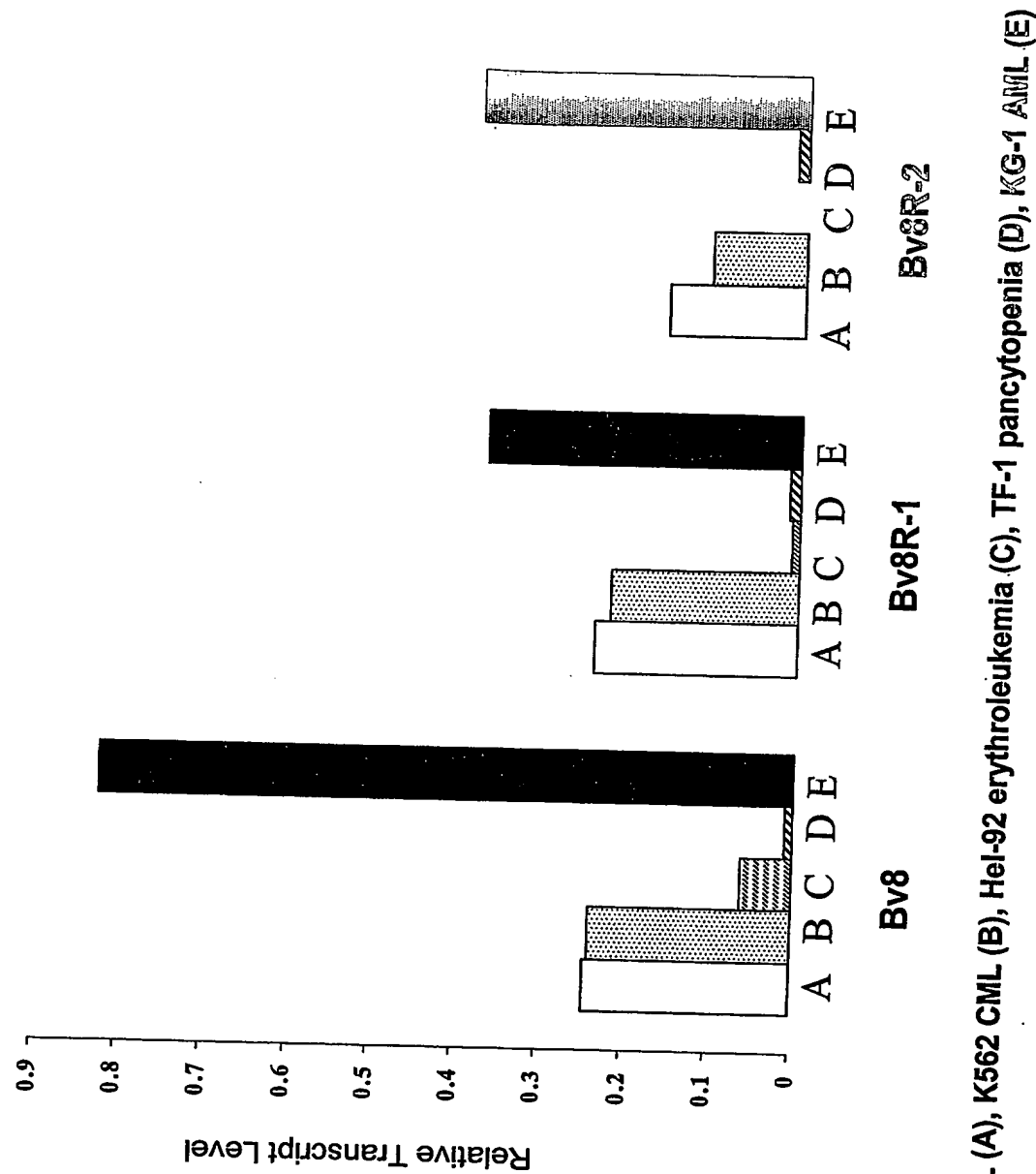
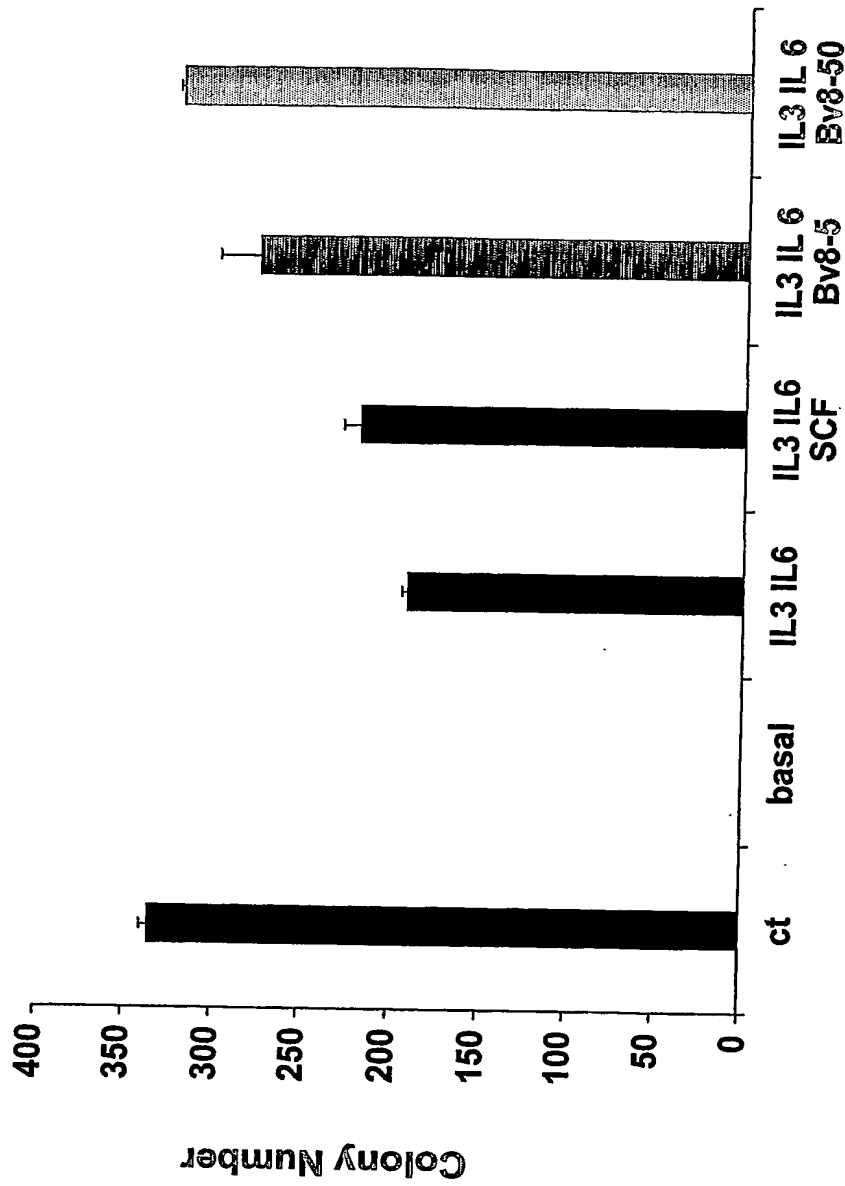


FIGURE 15D

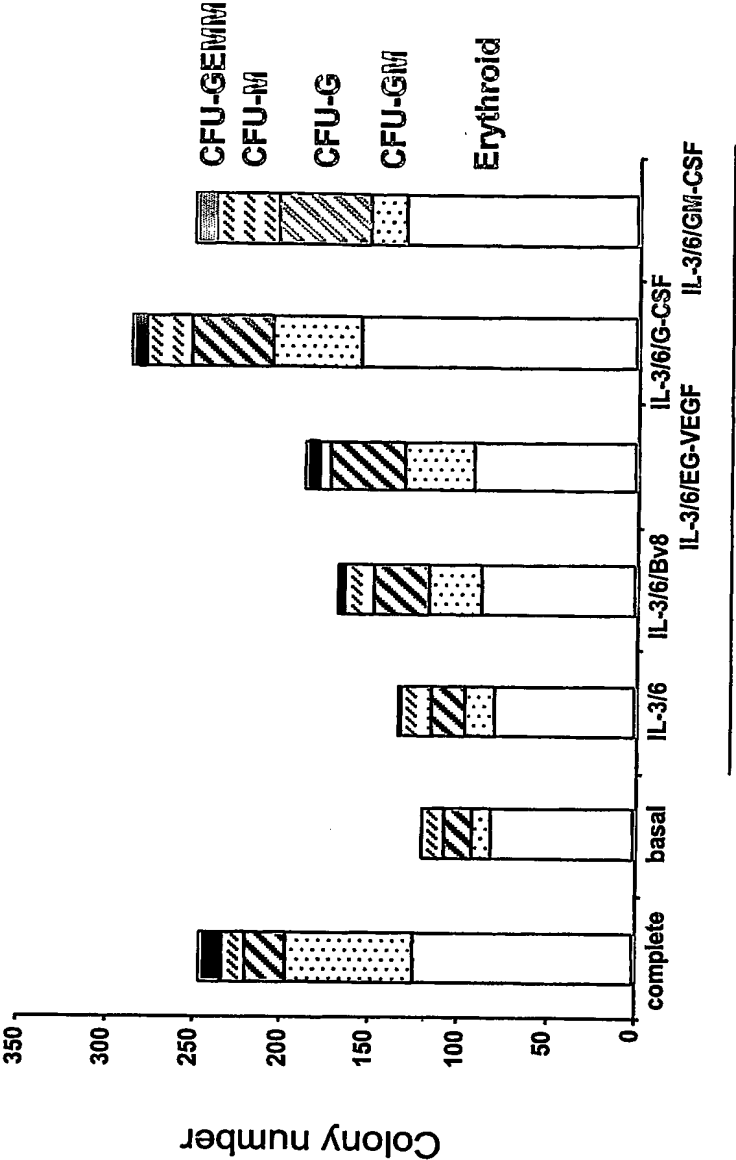


HL60 CML (A), K562 CML (B), Hel-92 erythroleukemia (C), TF-1 pancytopenia (D), KG-1 AML (E)

FIGURE 16



**FIGURE 17A**



basal

FIGURE 17B

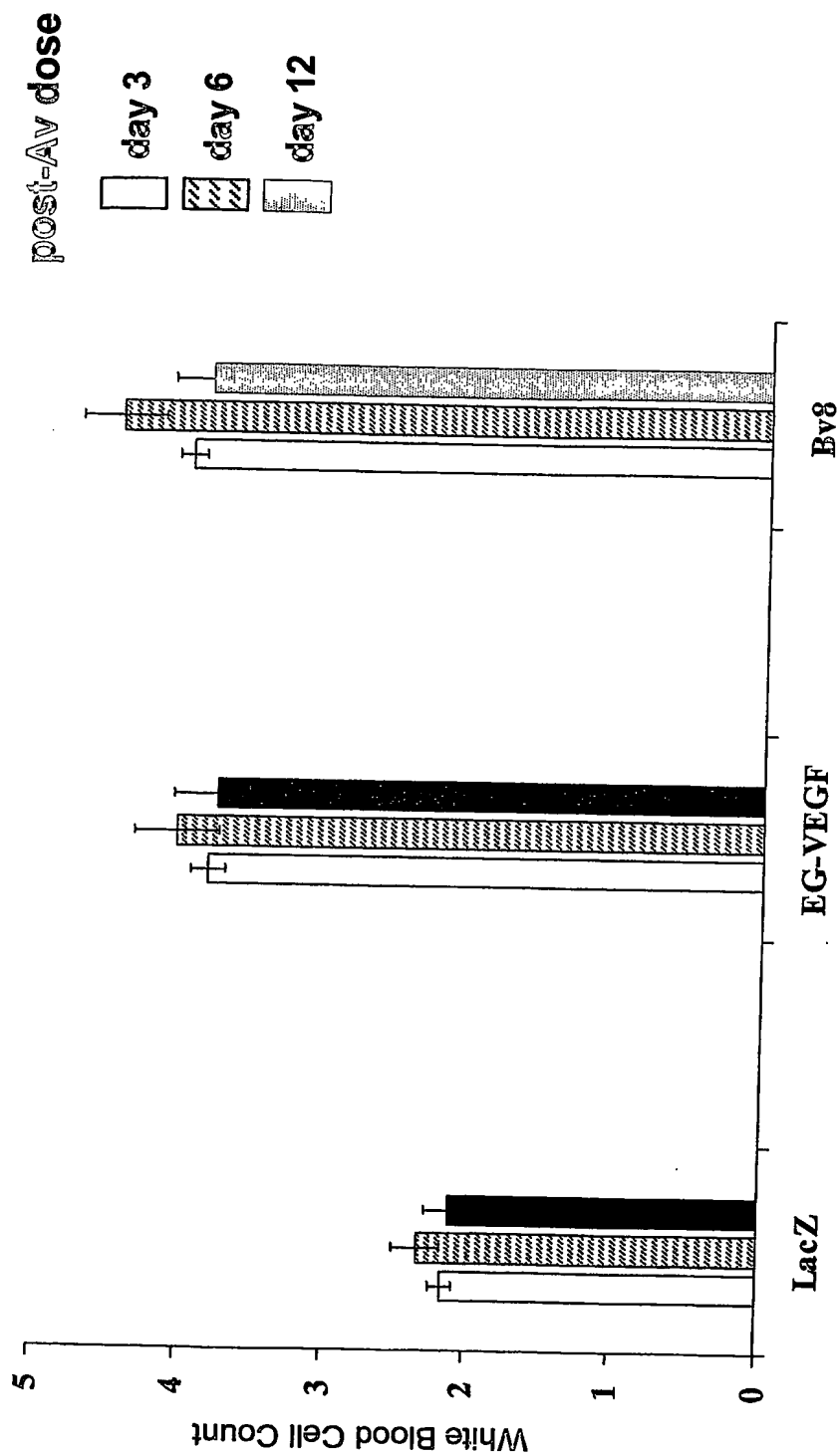


FIGURE 18

Figure 19A

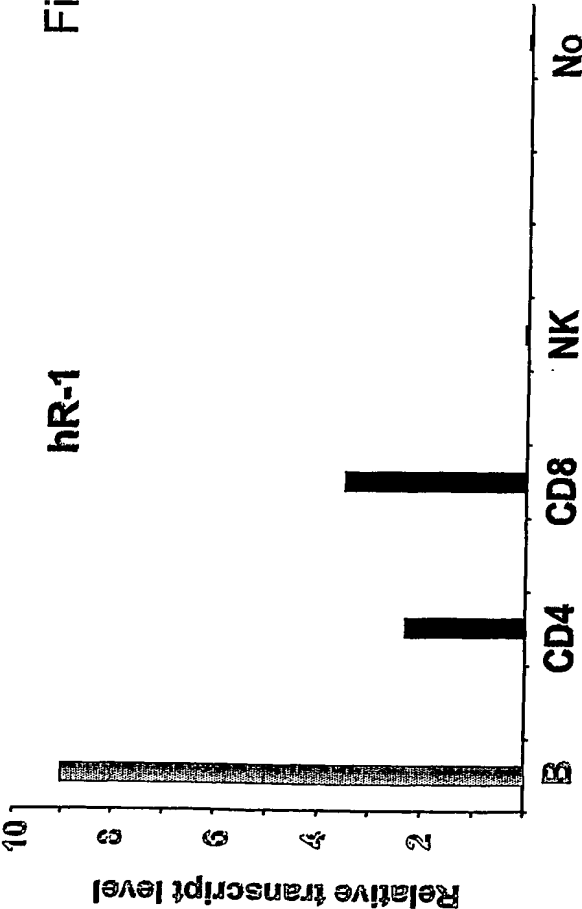


Figure 19B

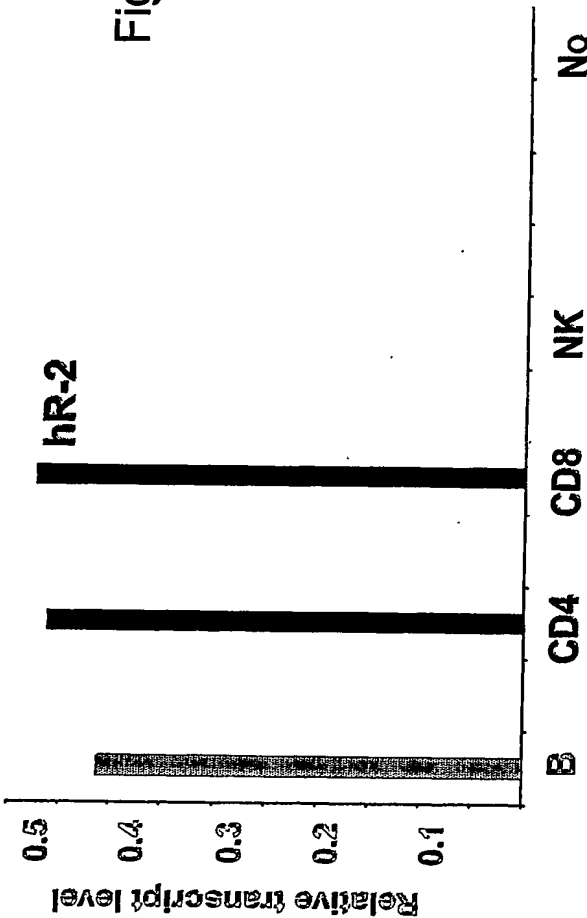
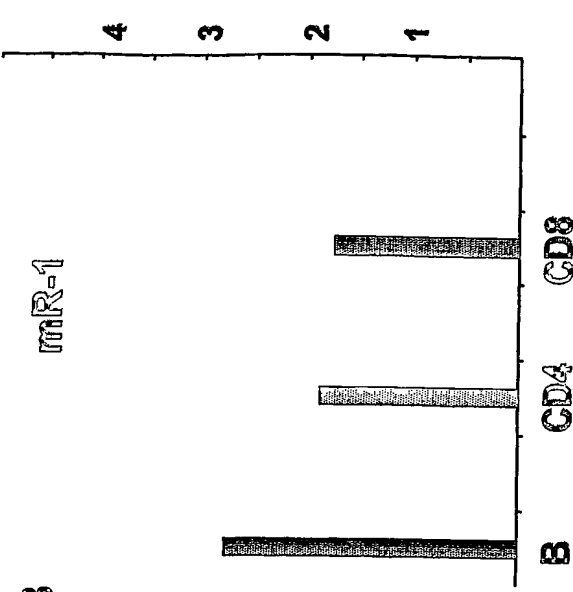


Figure 19D

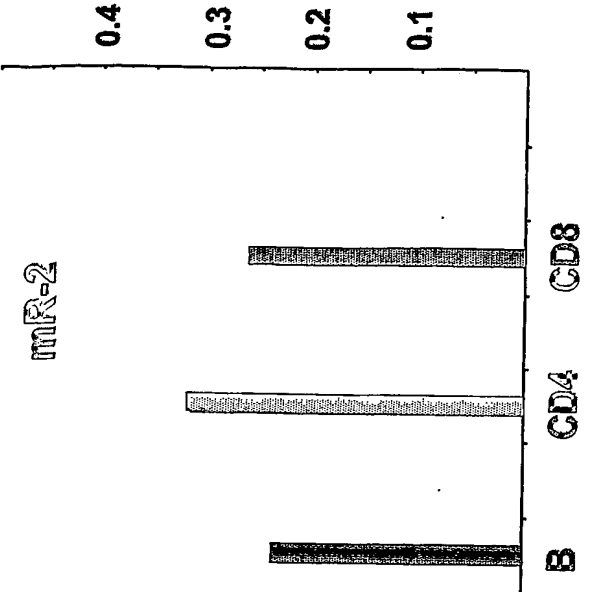


Figure 19C

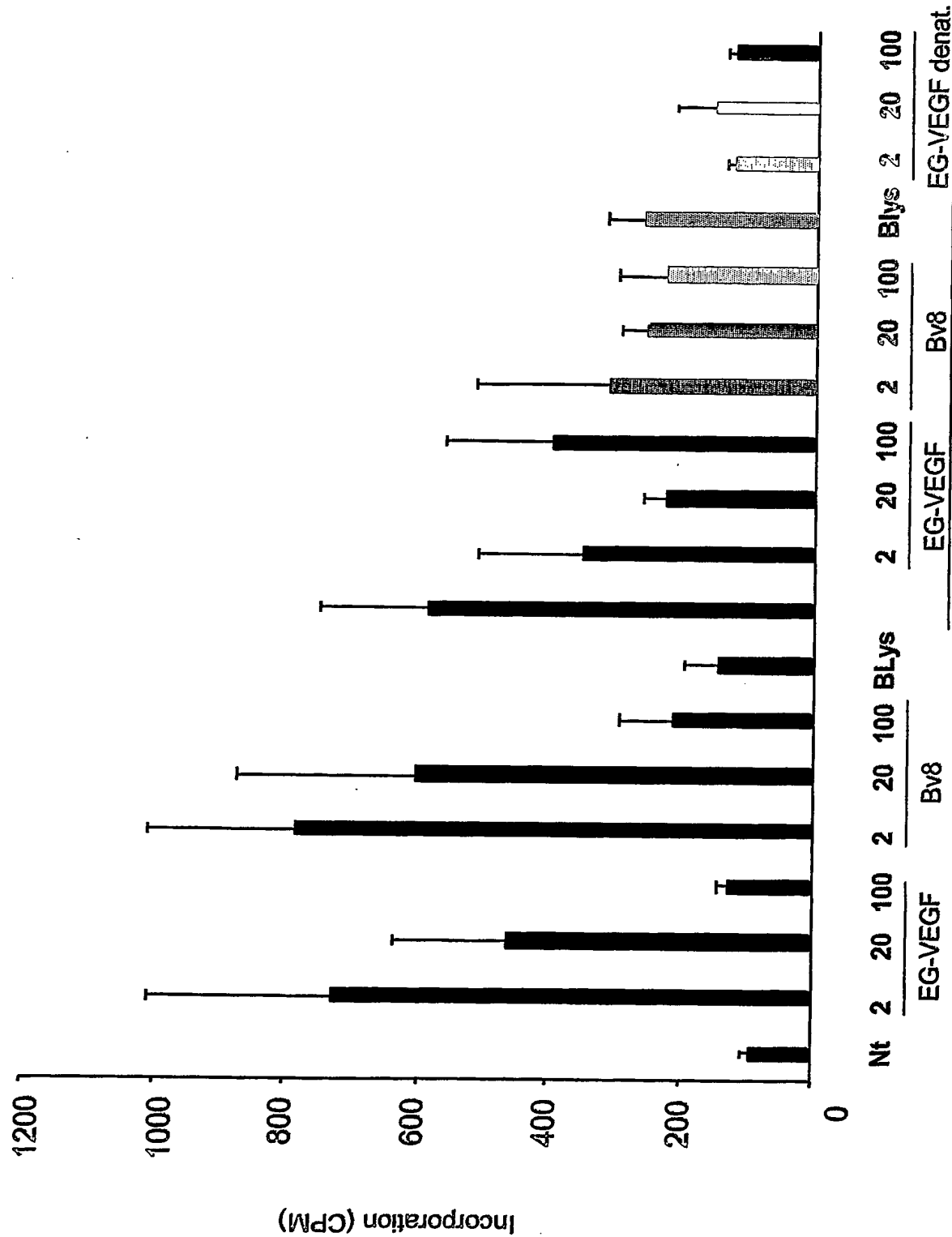


Figure 20 +  $\alpha$ -IgM



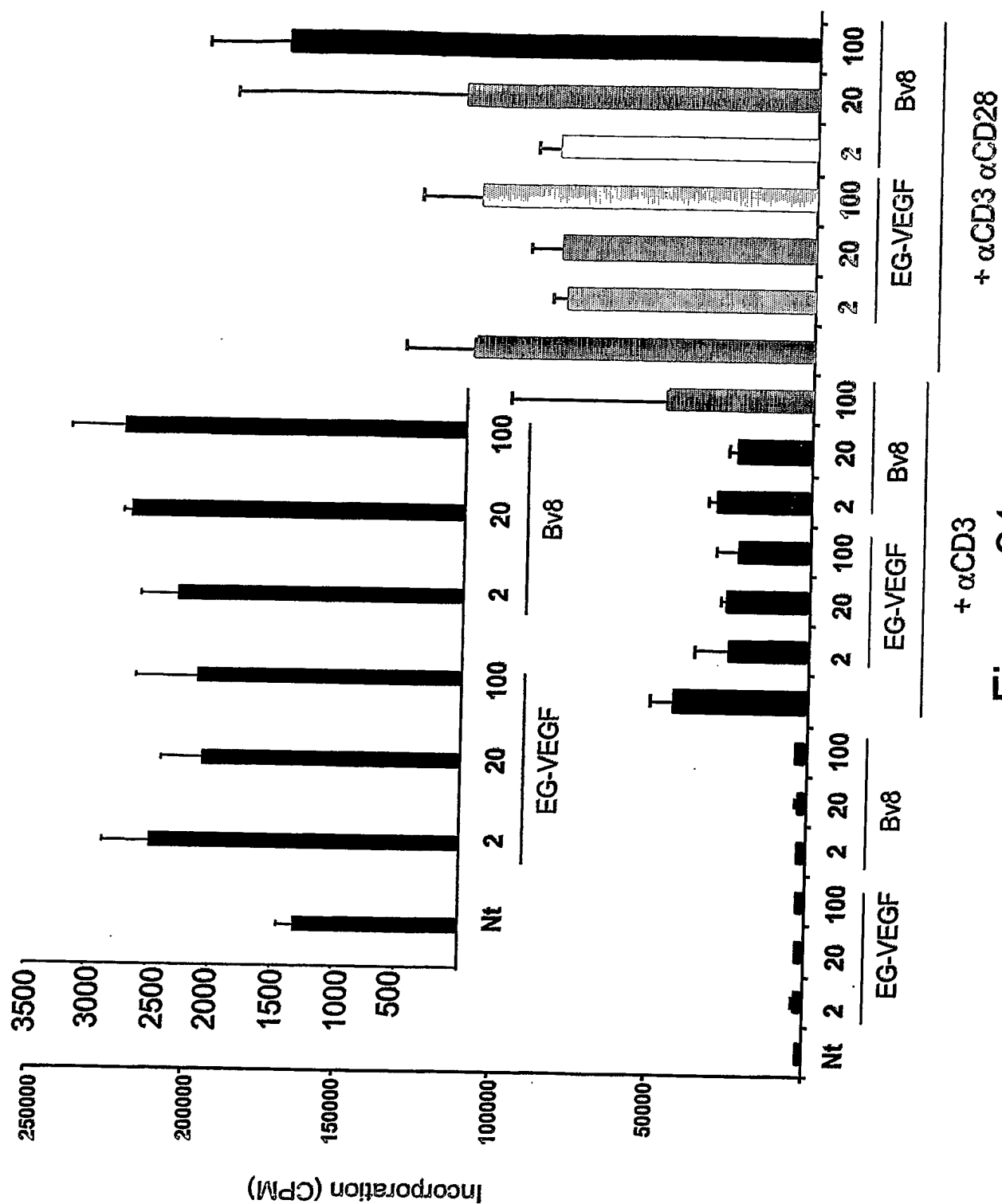


Figure 21

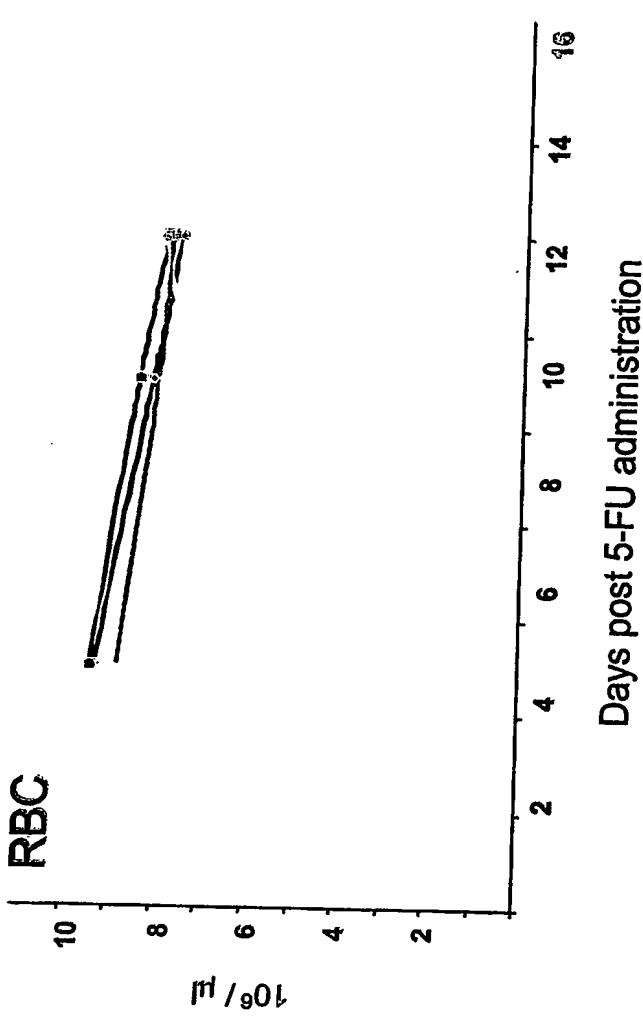
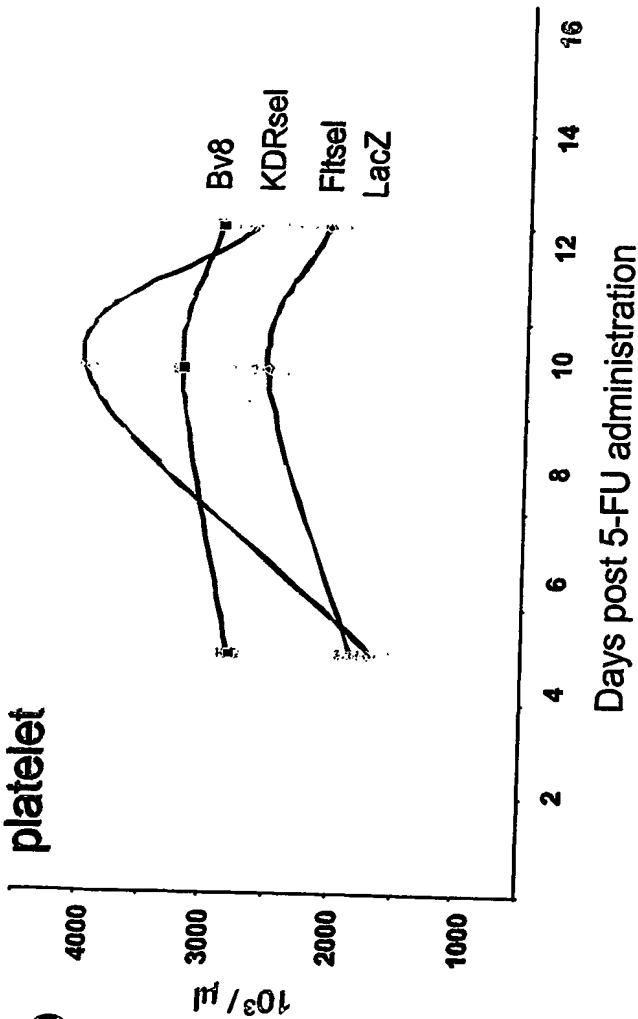


Figure 23D

Figure 23E

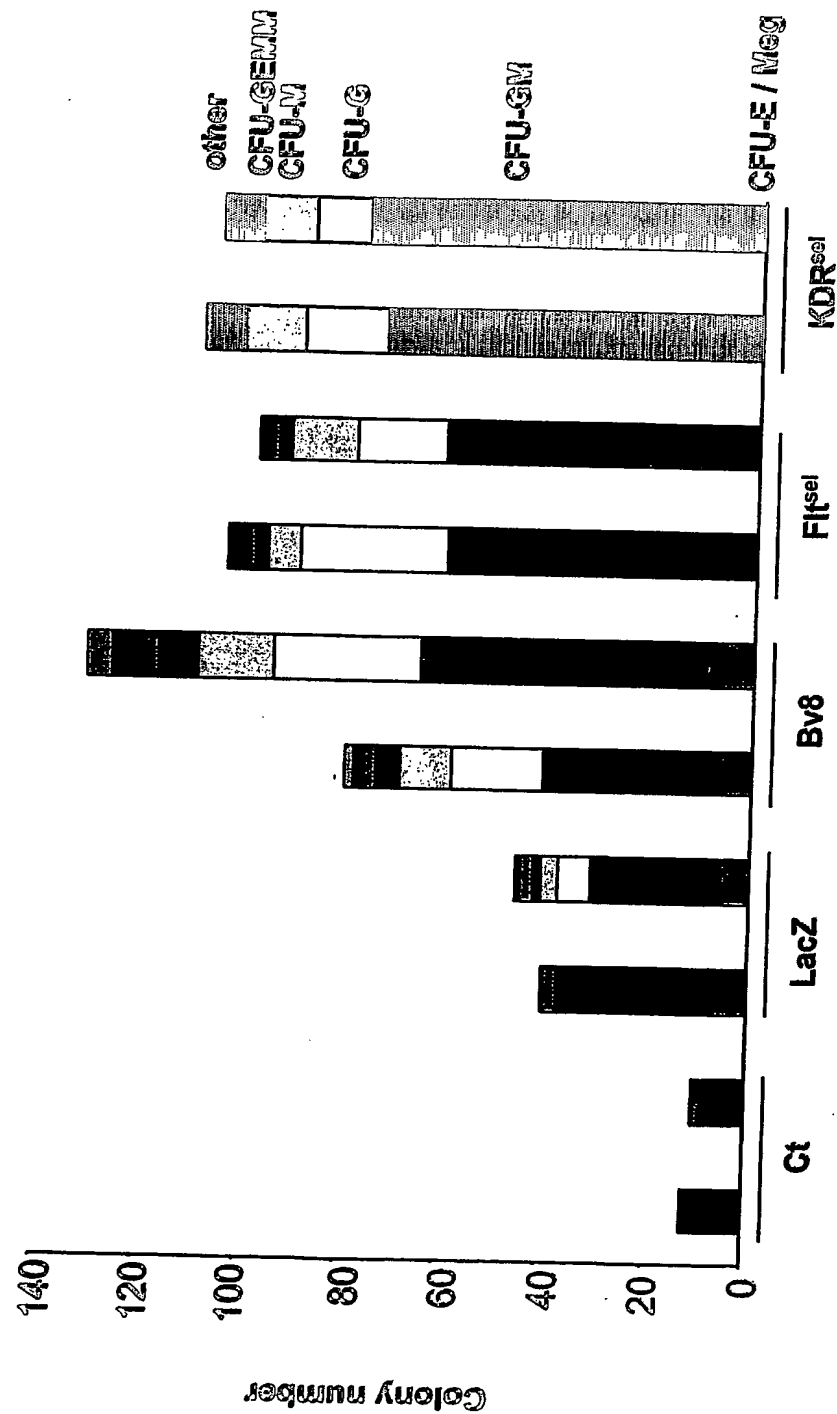


Figure 24